

Claims 1-34, 44-47 and 50-51 have been canceled.

Claim 35 has been amended as follows:

35. (Amended) A method of producing a zinc finger protein comprising:

Q54 (a) providing a database comprising designations for a plurality of zinc finger proteins, each protein comprising at least first, second and third fingers, and subdesignations for each of the three fingers of each of the zinc finger proteins;

a corresponding nucleic acid sequence for each zinc finger protein, each sequence comprising at least first, second and third triplets specifically bound by the at least first, second and third fingers respectively in each zinc finger protein, the first, second and third triplets being arranged in the nucleic acid sequence (3'-5') in the same respective order as the first, second and third fingers are arranged in the zinc finger protein (N-terminal to C-terminal);

(b) providing a target site for design of a zinc finger protein, the target site comprising contiguous first, second and third triplets in a 3'-5' order,

(c) for the first, second and third triplet in the target site, identifying first, second and third sets of zinc finger protein(s) in the database, the first set comprising zinc finger protein(s) comprising a finger specifically binding to the first triplet in the target site, the second set comprising zinc finger protein(s) comprising a finger specifically binding to the second triplet in the target site, the third set comprising zinc finger protein(s) comprising a finger specifically binding to the third triplet in the target site;

(d) outputting designations and subdesignations of the zinc finger proteins in the first, second, and third sets identified in step (c).

Claim 37 has been amended as follows:

Q53 37. (Amended) The method of claim 36 further comprising identifying subsets of the first, second and third sets, the subset of the first set comprising zinc finger protein(s) comprising a finger that specifically binds to the first triplet in the target site from the first finger position of a zinc finger protein in the database; the subset of the second set comprising zinc finger protein(s) comprising a finger that specifically binds to the second triplet in the target site from the second finger position in a zinc finger protein in the database; the subset of the third set comprising zinc finger protein(s) comprising a finger that specifically binds to the third triplet in the target site from a third finger position in a zinc finger protein in the database;

wherein

the outputting step comprises outputting designations and subdesignations of the subset of the first, second and third sets; and

the producing step comprises producing a zinc finger protein comprising a first finger from the first subset, a second finger from the second subset, and a third finger from the third subset.

Claim 41 has been amended as follows:

41. (Amended) The method of claim 35 wherein the target site is provided by

providing a target nucleic acid to be targeted by a zinc finger protein;
selecting a plurality of potential target sites within the target nucleic acid sequence;

evaluating whether each selected target site comprises 5'NNx aNY bNzc3; and
outputting a selected target site within the target nucleic acid comprising 5'NNx aNy bNzc3', the output selected target site providing the target site in step (b) of claim 35, wherein

each of (x, a), (y, b) and (z, c) is (N, N) or (G, K);
at least one of (x, a), (y, b) and (z, c) is (G, K). and
N and K are IUPAC-IUB ambiguity codes.

Claim 48 has been amended as follows:

48. (Amended) A computer program product for designing a zinc finger protein comprising:

(a) code for providing a database comprising
designations for a plurality of zinc finger proteins, each protein comprising at least first, second and third fingers ,
subdesignations for each of the three fingers of each of the zinc finger proteins;

a corresponding nucleic acid sequence for each zinc finger protein, each sequence comprising at least first, second and third triplets specifically bound by the at least first, second and third fingers respectively in each zinc finger protein, the first, second and third triplets being arranged in the nucleic acid sequence (3'-5') in the same respective order as the first, second and third fingers are arranged in the zinc finger protein (N-terminus to C-terminus);

(b) code for providing a target site for design of a zinc finger protein, the target site comprising at least first, second and third triplets,

(c) for the first, second and third triplet in the target site, code for identifying first, second and third sets of zinc finger protein(s) in the database, the first set comprising zinc finger protein(s) comprising a finger specifically binding to the first triplet in the target site, the second set comprising a finger specifically binding to the second triplet in the target site, the third set comprising a finger specifically binding to the third triplet in the target site;

(d) code for outputting designations and subdesignations of the zinc finger proteins in the first, second, and third sets identified in step (c).

(e) a computer readable storage medium for holding the codes.

Please add the following new claim:

52. The method of claim 35 wherein the target site is provided by providing a polynucleotide sequence;
selecting a potential target site within the polynucleotide sequence; the potential target site comprising contiguous first, second and third triplets of bases at first, second and third positions in the potential target site;
determining a plurality of subscores by applying a correspondence regime between triplets and triplet position in a sequence of three contiguous triplets, wherein each triplet has first, second and third corresponding positions, and each combination of triplet and triplet position has a particular subscore
calculating a score for the potential target site by combining subscores for the first, second, and third triplets;
repeating the selecting, determining and calculating steps at least once on a further potential target site comprising first, second and third triplets at first, second and third positions of the further potential target site to determine a further score;
providing output of at least one potential target site with its score, the at least one output potential target site providing the target site for step (b) in claim 35.

REMARKS

The pending claims are those designated Group II in the restriction requirement mailed March 12, 2001 in parent case 09/229,007. Claim 41 as filed was dependent on